STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _09/121,017β_

Source: _1Fw16_

Date Processed by STIC: _11/29/06_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER
VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
   http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
   Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>   <u>SUGGESTED CORRECTION</u>   SERIAL NUMBER: _09/121, 0178_   =

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
     Wrapped Aminos   was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
     prevent "wrapping."

2____Invalid Line Length The rules require that a line **not exceed 72** characters in length. This includes white spaces.

3____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
     Numbering   use **space characters**, instead.

4____Non-ASCII   The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please
ensure your subsequent submission is saved in ASCII text.**

5____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ✓__PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
    "bug"   ~~sequences(s)~~ √_____. Normally, PatentIn would automatically generate this section from the
1,3,5,17,19, ← previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
21,23,25,27,29   the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
Artificial or Unknown sequences.** *Suggestion: download PatentIn 3.4 from
USPTO website*

7____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence
     (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
    (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
    This sequence is intentionally skipped
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8____Skipped Sequences   Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
     (NEW RULES)   <210> sequence id number
    <400> sequence id number
    000

9____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
     (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
    In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10____Invalid <213>   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
     Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
    is Artificial Sequence. (see item 11 below)

11____Use of <220>   Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use
    of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."
    Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as
    explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of
    Sequence Rules

12_____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
     "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
    listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa   "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

IFW16

```
RAW SEQUENCE LISTING              DATE: 11/29/2006
PATENT APPLICATION: US/09/121,017B   TIME: 13:50:37

        Input Set : A:\sequence listing final.txt
        Output Set: N:\CRF4\11292006\I121017B.raw
```

Does Not Comply
Corrected Diskette Needed

see pr 1, 3-4, 6

```
  5 <110> APPLICANT: Imamura, Toru
  7         Asada, Masahiro
  9         Oka, Syuichi
 11         Suzuki, Masashi
 13         Yoneda, Atsuko
 15         Ota, Keiko
 17         Oda, Yuko
 19         Miyakawa, Kazuko
 21         Orikasa, Noriko
 23         Asada, Chie
 25         Kojima, Tetsuhito
 29 <120> TITLE OF INVENTION: HEPARIN-BINDING PROTEINS MODIFIED WITH SUGAR CHAINS,
 31         METHOD OF PRODUCING THE SAME AND PHARMACEUTICAL
 33         COMPOSITIONS CONTAINING THE SAME
 37 <130> FILE REFERENCE: 382.1019
 41 <140> CURRENT APPLICATION NUMBER: 09/121,017B
 43 <141> CURRENT FILING DATE: 1998-07-22
 47 <150> PRIOR APPLICATION NUMBER: 307721/1997
 49 <151> PRIOR FILING DATE: 1997-11-10
 53 <160> NUMBER OF SEQ ID NOS: 31
 57 <170> SOFTWARE: PatentIn Ver. 2.0
 61 <210> SEQ ID NO: 1
 63 <211> LENGTH: 221
 65 <212> TYPE: PRT
 67 <213> ORGANISM: Artificial Sequence
```

Suggestion: download PatentIn 3.4 from www.uspto.gov (USPTO website)

see p.6 and item 6 on Error Summary Sheet

```
W--> 71 <220> FEATURE:
W--> 71 <223> OTHER INFORMATION:
W--> 71 <400> 1
 73 Met Ala Pro Ala Arg Leu Phe Ala Leu Leu Leu Phe Phe Val Gly Gly
 75 1               5                   10                  15
 79 Val Ala Glu Ser Ile Arg Glu Thr Glu Val Ile Asp Pro Gln Asp Leu
 81             20                  25                  30
 85 Leu Glu Gly Arg Tyr Phe Ser Gly Ala Leu Pro Asp Asp Glu Asp Val
 87         35                  40                  45
 91 Val Gly Pro Gly Gln Glu Ser Asp Asp Phe Glu Leu Ser Gly Ser Gly
 93     50                  55                  60
 97 Asp Leu Asp Asp Leu Glu Asp Ser Met Ile Gly Pro Glu Val Val His
 99 65                  70                  75                  80
103 Pro Leu Val Pro Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu Leu Tyr
105             85                  90                  95
109 Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val
111             100                 105                 110
115 Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser
```

```
117          115                     120                     125
121 Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln
123      130                     135                     140
127 Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro
129 145                     150                     155                     160
133 Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn
135                     165                     170                     175
139 Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu
141              180                     185                     190
145 Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln
147         195                     200                     205
151 Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
153      210                     215                     220
159 <210> SEQ ID NO: 2
161 <211> LENGTH: 663
163 <212> TYPE: DNA
165 <213> ORGANISM: Artificial Sequence
169 <220> FEATURE:
171 <223> OTHER INFORMATION: Description of Artificial Sequence: fusion of
173       sequence for a part of human rydocan and a part of human fibroblast
175       growth factor 1
179 <220> FEATURE:
181 <221> NAME/KEY: CDS
183 <222> LOCATION: (1)..(663)
187 <400> SEQUENCE: 2
189 atg gcc ccc gcc cgt ctg ttc gcg ctg ctg ctg ttc ttc gta ggc gga    48
191 Met Ala Pro Ala Arg Leu Phe Ala Leu Leu Leu Phe Phe Val Gly Gly
193  1               5                  10                  15
197 gtc gcc gag tcg atc cga gag act gag gtc atc gac ccc cag gac ctc    96
199 Val Ala Glu Ser Ile Arg Glu Thr Glu Val Ile Asp Pro Gln Asp Leu
201              20                  25                  30
205 cta gaa ggc cga tac ttc tcc gga gcc cta cca gac gat gag gat gta   144
207 Leu Glu Gly Arg Tyr Phe Ser Gly Ala Leu Pro Asp Asp Glu Asp Val
209         35                  40                  45
213 gtg ggg ccc ggg cag gaa tct gat gac ttt gag ctg tct ggc tct gga   192
215 Val Gly Pro Gly Gln Glu Ser Asp Asp Phe Glu Leu Ser Gly Ser Gly
217      50                  55                  60
221 gat ctg gat gac ttg gaa gac tcc atg atc ggc cct gaa gtt gtc cat   240
223 Asp Leu Asp Asp Leu Glu Asp Ser Met Ile Gly Pro Glu Val Val His
225 65                  70                  75                  80
229 ccc ttg gtg cct cta gat gct aat tac aag aag ccc aaa ctc ctc tac   288
231 Pro Leu Val Pro Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu Leu Tyr
233                  85                  90                  95
237 tgt agc aac ggg ggc cac ttc ctg agg atc ctt ccg gat ggc aca gtg   336
239 Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val
241              100                 105                 110
245 gat ggg aca agg gac agg agc gac cag cac att cag ctg cag ctc agt   384
247 Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser
249         115                 120                 125
```

RAW SEQUENCE LISTING　　　　　　　DATE: 11/29/2006
PATENT APPLICATION: **US/09/121,017B**　　TIME: 13:50:37

Input Set : **A:\sequence listing final.txt**
Output Set: **N:\CRF4\11292006\I121017B.raw**

```
253 gcg gaa agc gtg ggg gag gtg tat ata aag agt acc gag act ggc cag     432
255 Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln
257       130                   135                   140
261 tac ttg gcc atg gac acc gac ggg ctt tta tac ggc tca cag aca cca     480
263 Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro
265 145                   150                   155                   160
269 aat gag gaa tgt ttg ttc ctg gaa agg ctg gag gag aac cat tac aac     528
271 Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn
273                   165                   170                   175
277 acc tat ata tcc aag aag cat gca gag aag aat tgg ttt gtt ggc ctc     576
279 Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu
281                   180                   185                   190
285 aag aag aat ggg agc tgc aaa cgc ggt cct cgg act cac tat ggc cag     624
287 Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln
289       195                   200                   205
293 aaa gca atc ttg ttt ctc ccc ctg cca gtc tct tct gat                 663
295 Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
297       210                   215                   220
303 <210> SEQ ID NO: 3
305 <211> LENGTH: 175
307 <212> TYPE: PRT
309 <212> ORGANISM: Artificial Sequence
```

W--> 313 <220> FEATURE:
W--> 313 <223> OTHER INFORMATION:
W--> 313 <400> 3

see p.6 and Errn Summary Sheet

```
315 Met Ser Arg Gly Ala Gly Arg Val Gln Gly Thr Leu Gln Ala Leu Val
317   1                   5                   10                   15
321 Phe Leu Gly Val Leu Val Gly Met Val Val Pro Ser Pro Ala Gly Ala
323                   20                   25                   30
327 Arg Ala Asn Gly Thr Leu Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu
329             35                   40                   45
333 Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly
335       50                   55                   60
339 Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln
341 65                   70                   75                   80
345 Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr
347                   85                   90                   95
351 Gly Gln Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln
353                   100                   105                   110
357 Thr Pro Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His
359             115                   120                   125
363 Tyr Asn Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val
365       130                   135                   140
369 Gly Leu Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr
371 145                   150                   155                   160
375 Gly Gln Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
377                   165                   170                   175
381 <210> SEQ ID NO: 4
383 <211> LENGTH: 525
```

RAW SEQUENCE LISTING   DATE: 11/29/2006
PATENT APPLICATION: US/09/121,017B   TIME: 13:50:38

Input Set : **A:\sequence listing final.txt**
Output Set: **N:\CRF4\11292006\I121017B.raw**

```
385 <212> TYPE: DNA
387 <213> ORGANISM: Artificial Sequence
391 <220> FEATURE:
393 <223> OTHER INFORMATION: Description of Artificial Sequence: fusion of
395       sequence for a part of mouse fibroblast growth factor 6 and
397       a part of human fibroblast growth factor 1
401 <220> FEATURE:
403 <221> NAME/KEY: CDS
405 <222> LOCATION: (1)..(525)
409 <400> SEQUENCE: 4
411 atg tcc cgg gga gca gga cgt gtt cag ggc acg ctg cag gct ctc gtc    48
413 Met Ser Arg Gly Ala Gly Arg Val Gln Gly Thr Leu Gln Ala Leu Val
415  1               5                  10                  15
419 ttc tta ggc gtc cta gtg ggc atg gtg gtg ccc tca cct gcc ggc gcc    96
421 Phe Leu Gly Val Leu Val Gly Met Val Val Pro Ser Pro Ala Gly Ala
423              20                  25                  30
427 cgc gcc aac ggc acg cta ctg gac gct aat tac aag aag ccc aaa ctc   144
429 Arg Ala Asn Gly Thr Leu Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu
431          35                  40                  45
435 ctc tac tgt agc aac ggg ggc cac ttc ctg agg atc ctt ccg gat ggc   192
437 Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly
439      50                  55                  60
443 aca gtg gat ggg aca agg gac agg agc gac cag cac att cag ctg cag   240
445 Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln
447  65                  70                  75                  80
451 ctc agt gcg gaa agc gtg ggg gag gtg tat ata aag agt acc gag act   288
453 Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr
455                  85                  90                  95
459 ggc cag tac ttg gcc atg gac acc gac ggg ctt tta tac ggc tca cag   336
461 Gly Gln Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln
463              100                 105                 110
467 aca cca aat gag gaa tgt ttg ttc ctg gaa agg ctg gag gag aac cat   384
469 Thr Pro Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His
471          115                 120                 125
475 tac aac acc tat ata tcc aag aag cat gca gag aag aat tgg ttt gtt   432
477 Tyr Asn Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val
479      130                 135                 140
483 ggc ctc aag aag aat ggg agc tgc aaa cgc ggt cct cgg act cac tat   480
485 Gly Leu Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr
487 145                 150                 155                 160
491 ggc cag aaa gca atc ttg ttt ctc ccc ctg cca gtc tct tct gat       525
493 Gly Gln Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
495              165                 170                 175
503 <210> SEQ ID NO: 5
505 <211> LENGTH: 181
507 <212> TYPE: PRT
509 <213> ORGANISM: Artificial Sequence
513 <220> FEATURE:
518 <223> OTHER INFORMATION:
```

W--> 513

W--> 518

see p. 6 and item 6 on Error Summary Sheet

this type of error appears in subsequent sequences

RAW SEQUENCE LISTING   DATE: 11/29/2006
PATENT APPLICATION: **US/09/121,017B**   TIME: 13:50:38

Input Set : **A:\sequence listing final.txt**
Output Set: **N:\CRF4\11292006\I121017B.raw**

```
W--> 513 <400> 5
    515 Met Ser Arg Gly Ala Gly Arg Val Gln Gly Thr Leu Gln Ala Leu Val
    517  1               5                  10                  15
    521 Phe Leu Gly Val Leu Val Gly Met Val Val Pro Ser Pro Ala Gly Ala
    523               20                  25                  30
    527 Arg Ala Gln Gly Thr Leu Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu
    529          35                  40                  45
    533 Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly
    535          50                  55                  60
    539 Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln
    541  65                  70                  75                  80
    545 Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr
    547               85                  90                  95
    551 Gly Gln Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln
    553              100                 105                 110
    557 Thr Pro Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Ala Ala
    559             115                 120                 125
    563 Thr Pro Ala Pro Asn His Tyr Asn Thr Tyr Ile Ser Lys Lys His Ala
    565            130                 135                 140
    569 Glu Lys Asn Trp Phe Val Gly Leu Lys Lys Asn Gly Ser Cys Lys Arg
    571 145                 150                 155                 160
    575 Gly Pro Arg Thr His Tyr Gly Gln Lys Ala Ile Leu Phe Leu Pro Leu
    577             165                 170                 175
    581 Pro Val Ser Ser Asp
    583              180
    589 <210> SEQ ID NO: 6
    591 <211> LENGTH: 543
    593 <212> TYPE: DNA
    595 <213> ORGANISM: Artificial Sequence
    599 <220> FEATURE:
    601 <223> OTHER INFORMATION: Description of Artificial Sequence: fusion of
    603       sequence for a part of mouse fibroblast growth factor 6,
    605       a part of human fibroblast growth factor 1 and an artificial
    607       sequence
    611 <220> FEATURE:
    613 <221> NAME/KEY: CDS
    615 <222> LOCATION: (1)..(543)
    619 <400> SEQUENCE: 6
    621 atg tcc cgg gga gca gga cgt gtt cag ggc acg ctg cag gct ctc gtc   48
    623 Met Ser Arg Gly Ala Gly Arg Val Gln Gly Thr Leu Gln Ala Leu Val
    625  1               5                  10                  15
    629 ttc tta ggc gtc cta gtg ggc atg gtg gtg ccc tca cct gcc ggc gcc   96
    631 Phe Leu Gly Val Leu Val Gly Met Val Val Pro Ser Pro Ala Gly Ala
    633               20                  25                  30
    637 cgc gcc caa ggc acg cta ctg gac gct aat tac aag aag ccc aaa ctc  144
    639 Arg Ala Gln Gly Thr Leu Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu
    641          35                  40                  45
    645 ctc tac tgt agc aac ggg ggc cac ttc ctg agg atc ctt ccg gat ggc  192
    647 Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 11/29/2006
PATENT APPLICATION: **US/09/121,017B**   TIME: 13:50:39

Input Set : **A:\sequence listing final.txt**
Output Set: **N:\CRF4\11292006\I121017B.raw**

Use of <220> Feature(NEW RULES):
Sequence(s)__are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or"Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:1,3,5,17,19,21,23,25,27,29

VERIFICATION SUMMARY DATE: 11/29/2006
PATENT APPLICATION: **US/09/121,017B** TIME: 13:50:39

Input Set : **A:\sequence listing final.txt**
Output Set: **N:\CRF4\11292006\I121017B.raw**

L:71 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:1, <213>
ORGANISM:Artificial Sequence
L:71 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:1, <213>
ORGANISM:Artificial Sequence
L:71 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:71
L:313 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:3, <213>
ORGANISM:Artificial Sequence
L:313 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:3, <213>
ORGANISM:Artificial Sequence
L:313 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:313
L:513 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:513 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:513 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:513
L:973 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:17, <213>
ORGANISM:Artificial Sequence
L:973 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:17, <213>
ORGANISM:Artificial Sequence
L:973 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:973
L:1201 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:19, <213>
ORGANISM:Artificial Sequence
L:1201 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:19, <213>
ORGANISM:Artificial Sequence
L:1201 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:19,Line#:1201
L:1431 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:21, <213>
ORGANISM:Artificial Sequence
L:1431 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:21, <213>
ORGANISM:Artificial Sequence
L:1431 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:1431
L:1701 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:23, <213>
ORGANISM:Artificial Sequence
L:1701 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:23, <213>
ORGANISM:Artificial Sequence
L:1701 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:23,Line#:1701
L:1999 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:25, <213>
ORGANISM:Artificial Sequence
L:1999 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:25, <213>
ORGANISM:Artificial Sequence
L:1999 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:25,Line#:1999
L:2199 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:27, <213>
ORGANISM:Artificial Sequence
L:2199 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:27, <213>
ORGANISM:Artificial Sequence
L:2199 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:2199
L:2441 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:29, <213>
ORGANISM:Artificial Sequence
L:2441 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:29, <213>
ORGANISM:Artificial Sequence
L:2441 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29,Line#:2441